



SEQUENCE LISTING

<110> Short, Jay M.
Kretz, Keith A.
Gray, Kevin A.
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Garrett, James B.
O' Donoghue, Eileen
Mathur, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES
THEREOF

<130> 564462001822

<140> US 09/866,379

<141> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

<160> 10

<170> FastSEQ for Windows Version 4.0

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<211> 1323

<212> DNA

<213> Escherichia coli

<220>

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<222> (1)...(1320)

<221> misc_feature

<222> 216

<223> n = A,T,C or G

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1				5					10					15		

ccg	caa	tct	gca	ttc	gct	cag	agt	gag	ccg	gag	ctg	aag	ctg	gaa	agt	96
Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
			20					25					30			

gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr 35 40 45	144
caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val 50 55 60	192
aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu 65 70 75 80	240
gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys 85 90 95	288
aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp 100 105 110	336
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro 115 120 125	384
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp 130 135 140	432
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala 145 150 155 160	480
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp 165 170 175	528
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu 180 185 190	576
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu 195 200 205	624
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala 210 215 220	672
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr 225 230 235 240	720
gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp 245 250 255	768
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	816

260	265	270	
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275 280 285			864
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His 290 295 300			912
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu 305 310 315 320			960
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu 325 330 335			1008
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly 340 345 350			1056
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln 355 360 365			1104
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp 370 375 380			1152
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr 385 390 395 400			1200
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala 405 410 415			1248
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu 420 425 430			1296
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 <213> Escherichia coli

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 20 25 30
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45

Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val
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Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu
65					70					75					80
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys
			85						90					95	
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp
			100					105					110		
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro
		115					120					125			
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp
	130					135					140				
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala
145					150					155					160
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp
				165					170						175
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu
			180					185					190		
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu
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Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala
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Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr
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Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp
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Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His
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Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser
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Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Met	Ala	Ala	Leu	Thr	Pro	His
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Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu
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Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly
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Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln
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Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp
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Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr
385				390						395					400
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala
			405						410					415	
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu
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<211> 49

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<213> Artificial Sequence

<220>

<223> primer

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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 4
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<210> 5
<211> 1901
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> 403
<223> n = A,T,C or G

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<210> 6

<211> 1901
 <212> DNA
 <213> Escherichia coli

<220>
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 <222> 403
 <223> n = A,T,C or G

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<210> 7
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 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (188)...(1483)

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tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa	180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	229
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro	
1 5 10	
tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg	277
Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu	
15 20 25 30	
gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag	325
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys	
35 40 45	
gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg	373
Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp	
50 55 60	
ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc	421
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala	
65 70 75	
tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg	469
Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu	
80 85 90	
gcg aaa aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat	517
Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp	
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Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu	
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ccc gat ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat	661
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp	
145 150 155	
aac gcg aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att	709
Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile	
160 165 170	
gct gac ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg	757
Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg	
175 180 185 190	
gtg ctt aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag	805
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195 200 205	
gac gaa agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg	853
Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val	
210 215 220	
agc gcc gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg	901
Ser Ala Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met	

225	230	235	
ctg acg gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg			949
Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro			
240	245	250	
ggg tgg gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt			997
Gly Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser			
255	260	265	270
ttg cat aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc			1045
Leu His Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala			
275	280	285	
cgc agc cgc gcc acc ccg tta tta gat ttg atc aag aca gcg ttg acg			1093
Arg Ser Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr			
290	295	300	
ccc cat cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca			1141
Pro His Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser			
305	310	315	
gtg ctg ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc			1189
Val Leu Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly			
320	325	330	
gca ctg gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg			1237
Ala Leu Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro			
335	340	345	350
cca ggt ggt gaa ctg gtg ttt gaa cgc tgg cgt ccg cta agc gat aac			1285
Pro Gly Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn			
355	360	365	
agc cag tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg			1333
Ser Gln Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met			
370	375	380	
cgt gat aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa			1381
Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys			
385	390	395	
ctg acc ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg			1429
Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser			
400	405	410	
ttg gca ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc			1477
Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys			
415	420	425	430
agt ttg taatgcataa aaaagagcat tcagttacct gaatgctctg aggctgatga			1533
Ser Leu			
caaacgaaga actgtctaata gcgtagaccg gaaaaggcgt tcacgccgca tccggccact			1593
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Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
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Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
85 90 95
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
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Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115 120 125
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
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Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145 150 155 160
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
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Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
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Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
210 215 220
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305 310 315 320
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
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Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
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Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
355 360 365
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
370 375 380
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
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Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
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Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45
caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta 192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
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aaa ctg ggt gag ctg aca ccg cgc ggt ggt gag cta atc gcc tat ctc 240
Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80
gga cat tac tgg cgt cag cgt ctg gta gcc gac gga ttg ctg cct aaa 288
Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys
85 90 95
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Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
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Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
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aac gcg caa ttt gat ttg cta caa cgc acg cca gag gtt gcc cgc agc Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275 280 285			864
cgc gcc acc ccg tta tta gat ttg atc aag aca gcg ttg acg ccc cat Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His 290 295 300			912
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gtg ctg Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu 305 310 315 320			960
ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu 325 330 335			1008
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly 340 345 350			1056
ggt gaa ctg gtg ttt gaa cgc tgg cgt ccg cta agc gat aac agc cag Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln 355 360 365			1104
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ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca			1248

Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415

ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg 1296
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 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
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 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
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 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys
 85 90 95
 Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
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 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
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 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
 145 150 155 160
 Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp
 165 170 175
 Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
 180 185 190
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
 195 200 205
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
 210 215 220
 Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 225 230 235 240
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu

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Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp		
	370					375					380						
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr		
385					390					395					400		
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Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu		
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Appendix A:

Atty Docket No.: 56446-20018.22/ 029006 / DIVER1370-7

SEQ ID NO:9 (Nov9x) and SEQ ID NO:7 (AppA, or wild type) alignment

Page 1 of 3

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	130	140	150	160	170	180	
Nov9x						1
AppA	tgatgcggcgcattagcatcgcacaggcaatcaataatgtcagatatgaaaagcggaaa						180
	190	200	210	220	230	240	
Nov9x						53
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	250	260	270	280	290	300	
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AppA	atctgcattcgcctcagagtgcgagcggagctgaagctggaaagtgtggtgattgtcagtcg						300
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Nov9x	tcatgggtgtgcgtgctccaaccaaggccacgcaactgatgcaggatgtcaccccagacgc						173
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Nov9x	atggccaacctggccggtaaaactgggtgagctgacaccgcgcgggtggtgagctaatacgc						233
AppA	atggccaacctggccggtaaaactgggtgagctgacaccgcgcgggtggtgagctaatacgc						420
	430	440	450	460	470	480	
Nov9x	ctatctcggacattactggcgtcagcgtctggttagccgacggattgctgctctaaatgtgg						293
AppA	ctatctcggacattacaaacgcagcgtctggttagccgacggattgctgctgcaaaaagg						480
	490	500	510	520	530	540	
Nov9x	ctgcccgcagctctggtcaggtcgcgattattgctgatgtcgacgagcgtaccgtaaaac						353
AppA	ctgcccgcagctctggtcaggtcgcgattattgctgatgtcgacgagcgtaccgtaaaac						540
	550	560	570	580	590	600	
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	610	620	630	640	650	660	
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AppA	agatacgtccagtcgccgatccggtattttaatcctctaaaaactggcggttgccaactgga						660
	670	680	690	700	710	720	

Page 2 of 3

[illegible]

Appendix A:

Atty Docket No.: 56446-20018.22/ 029006 / DIVER1370-7

SEQ ID NO:9 (Nov9x) and SEQ ID NO:7 (AppA, or wild type) alignment

Page 3 of 3

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	1390 1400 1410 1420 1430 1440	
Nov9x	actgaccctggcaggatgtgaagagcgaaatgcgcagggcatgtgttcggtggcaggttt	1253
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Nov9x	tacgcaaatacgtgaatgaagcacgcataccggcggtgcagtttgagatctcatcaccatca	1313
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AppA	cattcagttacctgaatgctctgaggctgatgacaaacgaagaactgtctaatacgctaga	1560
	1570 1580 1590 1600 1610 1620	
Nov9x		1323
AppA	cCGgaaaaggCGttcacgCGcatcCGgccactttcagttttcctctttctcggagtaac	1620
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Nov9x		1323
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AppA	tgaggatagcgcctttaatatTgacgcctgCctgttccagacgctgcattgacaaaactca	1740
	1750 1760 1770 1780 1790 1800	
Nov9x		1323
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	1810 1820 1830 1840 1850 1860	
Nov9x		1323
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	1870 1880 1890 1900	
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